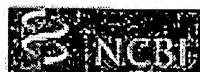


## Exhibit 1

Blast Result

Page 1 of 1



### Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

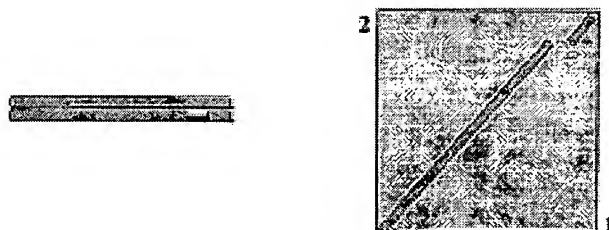
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.17 [Aug-19-2007]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **0** expect: **10.000** wordsize: **3** Filter: ☒ View option: **Standard**  
Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**  
☐ Show CDS translation **Align**

Sequence 1: unnamed protein product  
Length = 71 (1..71)

Sequence 2: unnamed protein product  
Length = 64 (1..64)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 94.0 bits (232), Expect = 2e-18  
Identities = 60/70 (85%), Positives = 61/70 (87%), Gaps = 7/70 (10%)  
Query 1: MVLRLSRKASVYVSKTNSGTNRACILIFLLLEFLLEFCTGDSVQSRKQRESCLTQ 60  
Subject 1: MVLRLSRKASVYVSKTNSGTNRACILIFLLLEFLLEFCTGDSVQSRKQRESCLTQ 60  
Query 61: IYSLPDKA 70 SEQ ID NO: 1  
Subject 57: ---ALPDKA 63 SEQ ID NO: 13

CPU time: 0.03 user secs, 0.01 sys. secs, 0.04 total secs.

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

8/27/2007